

Patent Application US/08/029,330

SEQUENCE LISTING

ENTERED

(1) GENERAL INFORMATION:

(i) APPLICANT: Burkly, Linda C.

(ii) TITLE OF INVENTION: Treatment for Insulin Dependent Diabetes

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Allegretti & Witcoff, Ltd.

(B) STREET: 10 South Wacker Drive, Suite 3000

(C) CITY: Chicago

(D) STATE: IL

(E) COUNTRY: US

(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 9 February 1993

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: McNicholas, Janet M.

(B) REGISTRATION NUMBER: 32,918

(C) REFERENCE/DOCKET NUMBER: 92,749; D015 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-715-1000

(B) TELEFAX: 312-715-1234

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy
chain variable region; amino acid 1 is Glu (E) but Gln (Q)

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may be substituted"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

48	GTC	AAA	CTG	CAG	CAG	TCT	GGG	GCA	GAG	CTT	GTG	AAG	CCA	GGG	GCC	TCA	
	Val	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	
	2				6					11					16		
96	GTC	AAG	TTG	TCC	TGC	ACA	GCT	TCT	GGC	TTC	AAC	ATT	AAA	GAC	ACC	TAT	
	Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	
				21					26					31			
144	ATG	CAC	TGG	GTG	AAG	CAG	AGG	CCT	GAA	CAG	GGC	CTG	GAG	TGG	ATT	GGA	
	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile	Gly	
			36				41						46				
192	AGG	ATT	GAT	CCT	GCG	AGT	GGC	GAT	ACT	AAA	TAT	GAC	CCG	AAG	TTC	CAG	
	Arg	Ile	Asp	Pro	Ala	Ser	Gly	Asp	Thr	Lys	Tyr	Asp	Pro	Lys	Phe	Gln	
		51					56					61					
240	GTC	AAG	GCC	ACT	ATT	ACA	GCG	GAC	ACG	TCC	TCC	AAC	ACA	GCC	TGG	CTG	
	Val	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Trp	Leu	
	66					71					76					81	
288	CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	ACT	GCC	GTC	TAC	TAC	TGT	GCA	
	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
					86				91						96		
336	GAC	GGA	ATG	TGG	GTA	TCA	ACG	GGA	TAT	GCT	CTG	GAC	TTC	TGG	GGC	CAA	
	Asp	Gly	Met	Trp	Val	Ser	Thr	Gly	Tyr	Ala	Leu	Asp	Phe	Trp	Gly	Gln	
				101				106						111			
360	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA									
	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser									
			116				121										

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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105 Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
106 2 6 11 16
107
108 Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
109 21 26 31
110
111 Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
112 36 41 46
113
114 Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
115 51 56 61
116
117 Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
118 66 71 76 81
119
120 Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
121 86 91 96
122
123 Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
124 101 106 111
125
126 Gly Thr Thr Val Thr Val Ser Ser
127 116 121
128

129 (2) INFORMATION FOR SEQ ID NO:3:
130
131 (i) SEQUENCE CHARACTERISTICS:
132 (A) LENGTH: 318 base pairs
133 (B) TYPE: nucleic acid
134 (C) STRANDEDNESS: double
135 (D) TOPOLOGY: linear
136
137 (ii) MOLECULE TYPE: cDNA
138
139 (ix) FEATURE:
140 (A) NAME/KEY: CDS
141 (B) LOCATION: 1..318
142 (D) OTHER INFORMATION: /product= "HP1/2 light chain
143 variable region"
144
145 (ix) FEATURE:
146 (A) NAME/KEY: misc_feature
147 (B) LOCATION: 1
148 (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light
149 chain variable region"
150
151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
152

153 AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA 48
154 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
155 1 5 10 15
156

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157	GAC	AGG	GTT	ACC	ATA	ACC	TGC	AAG	GCC	AGT	CAG	AGT	GTG	ACT	AAT	GAT	96
158	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Thr	Asn	Asp	
159				20					25					30			
160																	
161	GTA	GCT	TGG	TAC	CAA	CAG	AAG	CCA	GGG	CAG	TCT	CCT	AAA	CTG	CTG	ATA	144
162	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	
163			35					40					45				
164																	
165	TAT	TAT	GCA	TCC	AAT	CGC	TAC	ACT	GGA	GTC	CCT	GAT	CGC	TTC	ACT	GGC	192
166	Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	
167		50					55					60					
168																	
169	AGT	GGA	TAT	GGG	ACG	GAT	TTC	ACT	TTC	ACC	ATC	AGC	ACT	GTG	CAG	GCT	240
170	Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Thr	Val	Gln	Ala	
171	65					70					75					80	
172																	
173	GAA	GAC	CTG	GCA	GTT	TAT	TTC	TGT	CAG	CAG	GAT	TAT	AGC	TCT	CCG	TAC	288
174	Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys	Gln	Gln	Asp	Tyr	Ser	Ser	Pro	Tyr	
175					85				90						95		
176																	
177	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAG	ATC							318
178	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile							
179				100					105								
180																	
181	(2) INFORMATION FOR SEQ ID NO:4:																
182																	
183	(i) SEQUENCE CHARACTERISTICS:																
184	(A) LENGTH: 106 amino acids																
185	(B) TYPE: amino acid																
186	(D) TOPOLOGY: linear																
187																	
188	(ii) MOLECULE TYPE: protein																
189																	
190	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:																
191																	
192	Ser	Ile	Val	Met	Thr	Gln	Thr	Pro	Lys	Phe	Leu	Leu	Val	Ser	Ala	Gly	
193	1				5					10					15		
194																	
195	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Thr	Asn	Asp	
196				20					25					30			
197																	
198	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	
199			35					40					45				
200																	
201	Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	
202		50					55					60					
203																	
204	Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Thr	Val	Gln	Ala	
205	65					70					75					80	
206																	
207	Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys	Gln	Gln	Asp	Tyr	Ser	Ser	Pro	Tyr	
208					85				90						95		

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209
210 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
211 100 105
212
213 (2) INFORMATION FOR SEQ ID NO:5:
214
215 (i) SEQUENCE CHARACTERISTICS:
216 (A) LENGTH: 429 base pairs
217 (B) TYPE: nucleic acid
218 (C) STRANDEDNESS: single
219 (D) TOPOLOGY: linear
220
221 (ii) MOLECULE TYPE: cDNA
222
223 (ix) FEATURE:
224 (A) NAME/KEY: sig_peptide
225 (B) LOCATION: 1..57
226
227 (ix) FEATURE:
228 (A) NAME/KEY: mat_peptide
229 (B) LOCATION: 58..429
230
231 (ix) FEATURE:
232 (A) NAME/KEY: CDS
233 (B) LOCATION: 1..429
234
235 (ix) FEATURE:
236 (A) NAME/KEY: misc_feature
237 (B) LOCATION: 1
238 (D) OTHER INFORMATION: /note= "pBAG195 insert: AS heavy
239 chain variable region"
240
241 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
242
243 ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT 48
244 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
245 -19 -15 -10 -5
246
247 GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA 96
248 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
249 1 5 10
250
251
252 CCT AGC CAG ACC CTG AGC CTG ACC TGC ACC GCG TCT GGC TTC AAC ATT 144
253 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
254 15 20 25
255
256 AAA GAC ACC TAT ATG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT 192
257 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
258 30 35 40 45
259
260 GAG TGG ATT GGA AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC 240

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261 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
262 50 55 60
263
264 CCG AAG TTC CAG GTC AGA GTG ACA ATG CTG GTA GAC ACC AGC AGC AAC 288
265 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
266 65 70 75
267
268 CAG TTC AGC CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC 336
269 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
270 80 85 90
271
272 TAT TAT TGT GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC 384
273 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
274 95 100 105
275
276 TTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA GGT GAG TCC 429
277 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
278 110 115 120
279
280 (2) INFORMATION FOR SEQ ID NO:6:
281
282 (i) SEQUENCE CHARACTERISTICS:
283 (A) LENGTH: 143 amino acids
284 (B) TYPE: amino acid
285 (D) TOPOLOGY: linear
286
287 (ii) MOLECULE TYPE: protein
288
289 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
290
291 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
292 -19 -15 -10 -5
293
294 Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg
295 1 5 10
296
297 Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Ala Ser Gly Phe Asn Ile
298 15 20 25
299
300 Lys Asp Thr Tyr Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu
301 30 35 40 45
302
303
304 Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
305 50 55 60
306
307 Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
308 65 70 75
309
310 Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
311 80 85 90
312

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313 Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
314 95 100 105

315
316
317 Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
318 110 115 120

319
320 (2) INFORMATION FOR SEQ ID NO:7:

321
322 (i) SEQUENCE CHARACTERISTICS:

323 (A) LENGTH: 386 base pairs

324 (B) TYPE: nucleic acid

325 (C) STRANDEDNESS: single

326 (D) TOPOLOGY: linear

327

328 (ii) MOLECULE TYPE: cDNA

329

330 (ix) FEATURE:

331 (A) NAME/KEY: sig_peptide

332 (B) LOCATION: 1..57

333

334 (ix) FEATURE:

335 (A) NAME/KEY: mat_peptide

336 (B) LOCATION: 58..386

337

338 (ix) FEATURE:

339 (A) NAME/KEY: CDS

340 (B) LOCATION: 1..386

341

342 (ix) FEATURE:

343 (A) NAME/KEY: misc_feature

344 (B) LOCATION: 1

345 (D) OTHER INFORMATION: /note= "pBAG198 insert: VK2 (SVMDY)
346 light chain variable region"

347

348 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

349
350 ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT 48
351 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
352 -19 -15 -10 -5

353

354

355
356 GTC CAC TCC AGC ATC GTG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96
357 Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
358 1 5 10

359

360 AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AGT GTG 144
361 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
362 15 20 25

363

364 ACT AAT GAT GTA GCT TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG 192

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365 Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
366 30 35 40 45
367
368 CTG CTG ATC TAC TAT GCA TCC AAT CGC TAC ACT GGT GTG CCA GAT AGA 240
369 Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
370 50 55 60
371
372 TTC AGC GGT AGC GGT TAT GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288
373 Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
374 65 70 75
375
376 CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAG GAT TAT AGC 336
377 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
378 80 85 90
379
380 TCT CCG TAC ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT AAG TG 386
381 Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
382 95 100 105
383
384 (2) INFORMATION FOR SEQ ID NO:8:
385
386 (i) SEQUENCE CHARACTERISTICS:
387 (A) LENGTH: 128 amino acids
388 (B) TYPE: amino acid
389 (D) TOPOLOGY: linear
390
391 (ii) MOLECULE TYPE: protein
392
393 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
394
395 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
396 -19 -15 -10 -5
397
398 Val His Ser Ser Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
399 1 5 10
400
401 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val
402 15 20 25
403
404 Thr Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
405 30 35 40 45
406
407
408 Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
409 50 55 60
410
411 Phe Ser Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
412 65 70 75
413
414 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Ser
415 80 85 90
416

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417  Ser Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Lys
418          95              100              105
419

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SEQUENCE VERIFICATION REPORT
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S5136

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/08/029,330

DATE: 04/08/93
TIME: 07:46:22
S5136

LINE ORIGINAL TEXT

CORRECTED TEXT